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Sequence Listing was accepted.

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217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=9; day=16; hr=11; min=44; sec=31; ms=520;]

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Application No: 10815480

Version No: 2.0

Input Set:

Output Set:

Started: 2008-08-22 13:43:19.010

Finished: 2008-08-22 13:43:26.690

Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 680 ms

Total Warnings: 379

Total Errors: 0

No. of SeqIDs Defined: 919

Actual SeqID Count: 919

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
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Input Set:

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Actual SeqID Count: 919

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Young, Karen K. Y.

<120> Compositions and Methods for Detecting Certain
Flaviviruses, Including Members of the Japanese
Encephalitis Virus Serogroup

<130> 022101-000230US

<140> 10815480

<141> 2004-03-31

<150> US 60/459,491

<151> 2003-03-31

<150> US 60/552,454

<151> 2004-03-12

<150> US 60/555,530

<151> 2004-03-22

<160> 919

<170> FastSEQ for Windows Version 4.0

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region of the genomes of flaviviruses

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<213> Artificial Sequence

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 <400> 6
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 <210> 7
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<213> Artificial Sequence

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<223> Koutango virus Primer 1, region of conserved
sequence in 3' untranslated region of the genome
of Japanese encephalitis virus serogroup, KY1129

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<210> 8

<211> 25

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<223> Example Primer 1, Japanese encephalitis virus
serogroup amplification primer

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<210> 9

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

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region of the genomes of flaviviruses, consensus
sequence

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<210> 10

<211> 25

<212> DNA

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<223> Japanese encephalitis virus serogroup Primer 2

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<210> 13
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 amplification primer, region of conserved sequence in 3'
 untranslated region of the genome of Japanese encephalitis
 virus serogroup, KY1129

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<213> Artificial Sequence

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region of the genome of flaviviruses, KY1129

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<223> complement to SEQ ID NO:16

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<210> 18
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<223> probe for detecting flaviviruses, oligonucleotide
that hybridizes to conserved region of flaviviral
nucleic acid

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<223> n = g, c, t, a or absent

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<223> n = c, t, g or absent

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<221> modified_base
<222> (27)...(28)
<223> n = g, c, a, t or absent

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<210> 19
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<223> probe for detecting Japanese encephalitis virus
serogroup members

<400> 19
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<210> 20
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<220>
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<400> 20
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<210> 21
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<400> 21
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 <223> probe for detecting Murray Valley encephalitis virus

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<210> 23
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<220>
 <223> probe for detecting Kunjin virus

<400> 23
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<210> 24
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<220>
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<400> 24

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<210> 25

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> probe for detecting yellow fever virus

<400> 25

ggtctagagg ttagaggaga ccctccag 28

<210> 26

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> probe for detecting Montana myotis
leukencephalitis virus

<400> 26

ggactagagg ttagaggaga ccccttcc 28

<210> 27

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> probe for detecting Modoc virus

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ggactagagg ttgagggaga cccccggc 28

<210> 28

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Example Probe 1, Japanese encephalitis virus
serogroup amplification primer

<400> 28

ggactagagg ttagaggaga ccccgcg 28

<210> 29

<211> 418

<212> DNA

<213> St. Louis encephalitis virus

<220>

<223> 3' untranslated region of the genome of St. Louis
encephalitis virus (SLEV) isolate BFS1750

<400> 29

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ttgccaccgg atgtcaggta aacgggtgctg tctgtaacct ggccccaggt gactgggtta 60
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gtaggctgga gaggacgcaa aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag tgcgtgacca tggcgtaagg actagagggt agaggagacc ccgctgcaac 300
ttggcaaggc ccaaaccgc tcgaagctgt agagacgggg gaaggactag aggttagagg 360
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<210> 30

<211> 342

<212> DNA

<213> St. Louis encephalitis virus

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<223> 3' untranslated region of the genome of St. Louis
encephalitis virus (SLEV) isolate 1750-Std

<400> 30

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gtaggctgga gaggacgcaa aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
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<210> 31

<211> 418

<212> DNA

<213> St. Louis encephalitis virus

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<223> 3' untranslated region of the genome of St. Louis
encephalitis virus (SLEV) isolate TD6-4G

<400> 31

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gtaggctgga gaggacgcaa aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag tgcgtgacca tggcgtaagg actagagggt agaggagacc ccgctgcaac 300
tcggcaaggc ccaaaccgc tcgaagctgt agagatgggg gaaggactag aggttagagg 360
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<210> 32

<211> 342

<212> DNA

<213> St. Louis encephalitis virus

<220>

<223> 3' untranslated region of the genome of St. Louis
encephalitis virus (SLEV) isolate CoaV750

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ccaaagccaa tctggctgag tgcaaagccc ctcttccga ttcgggaggg tccctggcac 120
gtaggctgga gaggacgcaa aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgcgcaact 300
tggcaaggcc aaaaccgct cgaagctgta gagatggggg aa 342

<210> 33

<211> 418

<212> DNA

<213> St. Louis encephalitis virus

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<223> 3' untranslated region of the genome of St. Louis
encephalitis virus (SLEV) isolate L695121.05

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tcaaagccaa tccggctggg tgcaaagccc ctcttccga ctctgggaggg tccctggcat 120
gtaggctgga gaggacgcac aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgtaac 300
ttggcaaggc ccaaaccgc tcgaagctgt agagacgggg gaaggactag aggttagagg 360
agacccttg ccgttaacgc aaacaacagc atattgacac ctggaaagac aggagatc 418

<210> 34

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<212> DNA

<213> St. Louis encephalitis virus

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<223> 3' untranslated region of the genome of St. Louis
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<221> modified_base

<222> (384)...(384)

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gtaggctgga gaggacgcac aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag agcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgtaac 300
ttggcaaggc ccaaaccgc tcgaagctgt agagacgggg gaaggactag aggttagagg 360
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<210> 35

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<213> St. Louis encephalitis virus

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encephalitis virus (SLEV) isolate MSI-7

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gtaggctgga gaggacgcac aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag tgcgtgacca tggcgtaagg actagagggt agaggagacc ccgctgtaac 300
ttggcaaggc ccaaaccgcg tcaaagctgt agagacgggg gaaggactag aggttagagg 360
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<213> St. Louis encephalitis virus

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<223> 3' untranslated region of the genome of St. Louis
encephalitis virus (SLEV) isolate Kern217

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tggagaggac gcacaagtca gaccagaaat gccacctgaa agcatgctaa aggtgctgtc 180
tgtacatgcc ccaggaggac tgggttaaca aagcttaaca gccccagcgg cccaaaccat 240
ggagtgcgtg accatggcgt aaggactaga ggtagagga gaccccgctg taacttggca 300
aggcccaaac ccgtcaaag ctgtagagac gggggaagga ctagaggtta gaggagacc 360
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<210> 37

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<213> St. Louis encephalitis virus

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<223> 3' untranslated region of the genome of St. Louis
encephalitis virus (SLEV) isolate CoaV608

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gaaagcatgc taaaggtgct gtctgtacat gcccaggag gactgggtta acaaagctta 180
acagccccag cggcccaaac catggagtgc gtgacctgg cgtaaggact agaggttaga 240
ggagaccccg ctgtaacttg gcaaggccca aaccgctca aagctgtaga gacgggggaa 300
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encephalitis virus (SLEV) isolate TBH-28

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gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag tgcgtgacca tggcgtaagg actagagggt agaggagacc ccgctgtaat 300
ttggcaaggc ccaaaccgcg tcgaagctgt agagacgggg gaaggactag aggttagagg 360
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<211> 402

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tggagcggac gcacaagtca gaccagaaat gccacctgaa agcatgctaa aggtgctgtc 180
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ggagtgcgtg accatggcgt aaggactaga ggtagagga gaccccgctg taacttggca 300
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<210> 40

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gaaagcatgc taaagggtgct gtctgtacat gccccaggag gactgggtta acaaagctta 180
acagccccag cggcccaaac catggagtgc gtgacctgg cgtaaggact agaggttaga 240
ggagaccccg ctgcaacttg gcaaggccca aaccgctcg aagctgtaga gacgggggaa 300
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<223> Dengue virus consensus upstream primer

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<210> 42

<211> 27

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<210> 43

<211> 27

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<223> n = methyl-dA

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<222> (27)...(27)

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<223> Dengue virus type I upstream primer

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